

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/563,601
Source: IFWP
Date Processed by STIC: 1/19/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 01/19/2006

PATENT APPLICATION: US/10/563,601

TIME: 13:27:45

Input Set : E:\2003-005.txt

Output Set: N:\CRF4\01192006\J563601.raw

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3 <110> APPLICANT: AKZO Nobel NV
5 <120> TITLE OF INVENTION: Babesia vaccines
W--> 7 <130> FILE REFERENCE:
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/563,601
C--> 9 <141> CURRENT FILING DATE: 2006-01-06
9 <160> NUMBER OF SEQ ID NOS: 19
11 <170> SOFTWARE: PatentIn version 3.3
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 852
15 <212> TYPE: DNA
16 <213> ORGANISM: Babesia canis
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (50)..(820)
23 <400> SEQUENCE: 1
24 agtcgatacc tccgagaata gtcttgatt aatcctgtcg ctattcaca atg aag ggt      58
25                                     Met Lys Gly
26                                     1
28 ttc ttc gga att att ttg tcc att att ttt gtt cgt gcc gtt agc tgc      106
29 Phe Phe Gly Ile Ile Leu Ser Ile Ile Phe Val Arg Ala Val Ser Cys
30      5                      10                      15
32 act gag gat gag aaa agg gat agt gtc gtc gag ggc gct acg tcc gtt      154
33 Thr Glu Asp Glu Lys Arg Asp Ser Val Val Glu Gly Ala Thr Ser Val
34 20                      25                      30                      35
36 gaa gcc agc tta aag gag cag atc gac tgg ctc gct gaa cgt tat tcc      202
37 Glu Ala Ser Leu Lys Glu Gln Ile Asp Trp Leu Ala Glu Arg Tyr Ser
38      40                      45                      50
40 gct gac ttg act aac aaa gac act tca aaa tgg aat acc gac gag aag      250
41 Ala Asp Leu Thr Asn Lys Asp Thr Ser Lys Trp Asn Thr Asp Glu Lys
42      55                      60                      65
44 gtg aag gag ctg ttg aat gag aag gct gtt ggc ata gag tct cgc ctt      298
45 Val Lys Glu Leu Leu Asn Glu Lys Ala Val Gly Ile Glu Ser Arg Leu
46      70                      75                      80
48 ctt gcc att gct aag gaa ttc cac aaa ttg aag tcc gtt ctg tgc acc      346
49 Leu Ala Ile Ala Lys Glu Phe His Lys Leu Lys Ser Val Leu Cys Thr
50      85                      90                      95
52 ggc gtc aac gaa act ccc gct cat gtc gct aac agg gtg tca ccc gga      394
53 Gly Val Asn Glu Thr Pro Ala His Val Ala Asn Arg Val Ser Pro Gly
54 100                      105                      110                      115
56 gac gcc atc tcc atg ctc tac gtg ctt tct atc act cac agg gaa ttg      442
57 Asp Ala Ile Ser Met Leu Tyr Val Leu Ser Ile Thr His Arg Glu Leu
58      120                      125                      130
60 tct agc ctt aag aat aag atc gat gaa tgg aag aag gtc aag gca tct      490

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61 Ser Ser Leu Lys Asn Lys Ile Asp Glu Trp Lys Lys Val Lys Ala Ser
62          135          140          145
64 gaa gat ggc acc aaa gtg atc caa aat atc aag gac gac agg act aac      538
65 Glu Asp Gly Thr Lys Val Ile Gln Asn Ile Lys Asp Asp Arg Thr Asn
66          150          155          160
68 acc tgg ttc gtt gcc cat gga ttc aag gta gct gag ctc aac gat gtc      586
69 Thr Trp Phe Val Ala His Gly Phe Lys Val Ala Glu Leu Asn Asp Val
70          165          170          175
72 acc ctt gag aaa ctt gca aca gtg gtt aac gaa ttg gtg tcc cac aaa      634
73 Thr Leu Glu Lys Leu Ala Thr Val Val Asn Glu Leu Val Ser His Lys
74 180          185          190          195
76 gat atg att tac att aac gac gct atg aag caa aac gtt gat aaa tgg      682
77 Asp Met Ile Tyr Ile Asn Asp Ala Met Lys Gln Asn Val Asp Lys Trp
78          200          205          210
80 acc aag gag gag tct gaa aga ttg gcc atg atg gct gaa cag ggt ata      730
81 Thr Lys Glu Glu Ser Glu Arg Leu Ala Met Met Ala Glu Gln Gly Ile
82          215          220          225
84 tct gga gcc aag ggt aag aag gat gga ttc tca ttc gcc ggt ctt agt      778
85 Ser Gly Ala Lys Gly Lys Lys Asp Gly Phe Ser Phe Ala Gly Leu Ser
86          230          235          240
88 gtc atc agc ctt ctt gtt gcc gcc gtc gcg gtt gtg gtc taa      820
89 Val Ile Ser Leu Leu Val Ala Ala Val Ala Val Val Val
90          245          250          255
92 gaggttaagg atgactatatt gtgggcgtaa tg      852
95 <210> SEQ ID NO: 2
96 <211> LENGTH: 256
97 <212> TYPE: PRT
98 <213> ORGANISM: Babesia canis
100 <400> SEQUENCE: 2
102 Met Lys Gly Phe Phe Gly Ile Ile Leu Ser Ile Ile Phe Val Arg Ala
103 1          5          10          15
106 Val Ser Cys Thr Glu Asp Glu Lys Arg Asp Ser Val Val Glu Gly Ala
107          20          25          30
110 Thr Ser Val Glu Ala Ser Leu Lys Glu Gln Ile Asp Trp Leu Ala Glu
111          35          40          45
114 Arg Tyr Ser Ala Asp Leu Thr Asn Lys Asp Thr Ser Lys Trp Asn Thr
115          50          55          60
118 Asp Glu Lys Val Lys Glu Leu Leu Asn Glu Lys Ala Val Gly Ile Glu
119 65          70          75          80
122 Ser Arg Leu Leu Ala Ile Ala Lys Glu Phe His Lys Leu Lys Ser Val
123          85          90          95
126 Leu Cys Thr Gly Val Asn Glu Thr Pro Ala His Val Ala Asn Arg Val
127          100          105          110
130 Ser Pro Gly Asp Ala Ile Ser Met Leu Tyr Val Leu Ser Ile Thr His
131          115          120          125
134 Arg Glu Leu Ser Ser Leu Lys Asn Lys Ile Asp Glu Trp Lys Lys Val
135          130          135          140
138 Lys Ala Ser Glu Asp Gly Thr Lys Val Ile Gln Asn Ile Lys Asp Asp
139 145          150          155          160

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142 Arg Thr Asn Thr Trp Phe Val Ala His Gly Phe Lys Val Ala Glu Leu
143                               165                               170                               175
146 Asn Asp Val Thr Leu Glu Lys Leu Ala Thr Val Val Asn Glu Leu Val
147                               180                               185                               190
150 Ser His Lys Asp Met Ile Tyr Ile Asn Asp Ala Met Lys Gln Asn Val
151                               195                               200                               205
154 Asp Lys Trp Thr Lys Glu Glu Ser Glu Arg Leu Ala Met Met Ala Glu
155                               210                               215                               220
158 Gln Gly Ile Ser Gly Ala Lys Gly Lys Lys Asp Gly Phe Ser Phe Ala
159 225                               230                               235                               240
162 Gly Leu Ser Val Ile Ser Leu Leu Val Ala Ala Val Ala Val Val Val
163                               245                               250                               255
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 845
168 <212> TYPE: DNA
169 <213> ORGANISM: Babesia canis
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (2)..(784)
176 <400> SEQUENCE: 3
177 a gtc gat acc tcc gag aat agt ctt gta tta atc ctg tcg cta ttc aca      49
178   Val Asp Thr Ser Glu Asn Ser Leu Val Leu Ile Leu Ser Leu Phe Thr
179   1                               5                               10                               15
181 atg aag ggt ttc ttc gga att att ttg tct att att ttc gtt cgt gcc      97
182 Met Lys Gly Phe Phe Gly Ile Ile Leu Ser Ile Ile Phe Val Arg Ala
183                               20                               25                               30
185 gtt agc tgc act gag gat gag aac agg gat agt gtc gtc gag ggc gct      145
186 Val Ser Cys Thr Glu Asp Glu Asn Arg Asp Ser Val Val Glu Gly Ala
187                               35                               40                               45
189 acg tcc gtt gaa gcc agc tta aag gag cag atc gac tgg ctc gct gaa      193
190 Thr Ser Val Glu Ala Ser Leu Lys Glu Gln Ile Asp Trp Leu Ala Glu
191                               50                               55                               60
193 cgt tat tcc gct gac ttg act aac aaa gac act tca aaa tgg aat acc      241
194 Arg Tyr Ser Ala Asp Leu Thr Asn Lys Asp Thr Ser Lys Trp Asn Thr
195 65                               70                               75                               80
197 gaa gag cag gtg aag gag ctg ttg aat gag aag gct gtt ggc ata gag      289
198 Glu Glu Gln Val Lys Glu Leu Leu Asn Glu Lys Ala Val Gly Ile Glu
199                               85                               90                               95
201 tct cgc ctt ctt gcc att gct aag gag ttc cac aaa ttg aag tcc gtt      337
202 Ser Arg Leu Leu Ala Ile Ala Lys Glu Phe His Lys Leu Lys Ser Val
203                               100                              105                              110
205 ctg tgc acc ggc gtc aac gaa act ccc gct cat gtc gct aac agg gtg      385
206 Leu Cys Thr Gly Val Asn Glu Thr Pro Ala His Val Ala Asn Arg Val
207                               115                              120                              125
209 tca ccc gga gac gcc atc tcc atg ctt tac gtg ctt cct aac act cac      433
210 Ser Pro Gly Asp Ala Ile Ser Met Leu Tyr Val Leu Pro Asn Thr His
211                               130                              135                              140
213 agg gaa ttg tct agc ctt aag aat aag atc gat gaa tgg aag aag gtc      481
214 Arg Glu Leu Ser Ser Leu Lys Asn Lys Ile Asp Glu Trp Lys Lys Val

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```

215 145          150          155          160
217 aag gca tct gac aat ggc acc aat gtg atc aaa aat atc aag gac gac      529
218 Lys Ala Ser Asp Asn Gly Thr Asn Val Ile Lys Asn Ile Lys Asp Asp
219          165          170          175
221 agg act aac acc tgg ttc gtt gcc cat gga ttc aag gta gct gag ctc      577
222 Arg Thr Asn Thr Trp Phe Val Ala His Gly Phe Lys Val Ala Glu Leu
223          180          185          190
225 aac gat gta acc ctt gag aaa ctt gca aca gtg gtt aaa aaa ttg gtg      625
226 Asn Asp Val Thr Leu Glu Lys Leu Ala Thr Val Val Lys Lys Leu Val
227          195          200          205
229 tcc cac aaa gat atg aaa tac att aac aaa gtt atg aaa aaa tat ttt      673
230 Ser His Lys Asp Met Lys Tyr Ile Asn Lys Val Met Lys Lys Tyr Phe
231          210          215          220
233 gac agg cag aaa aag gag gct gaa aga ttg acc aaa aag gcc gag aag      721
234 Asp Arg Gln Lys Lys Glu Ala Glu Arg Leu Thr Lys Lys Ala Glu Lys
235 225          230          235          240
237 ggt atg tct gga ggt aag tat aag gtg aaa ggt tat gca gcc ccc tct      769
238 Gly Met Ser Gly Gly Lys Tyr Lys Val Lys Gly Tyr Ala Ala Pro Ser
239          245          250          255
241 act tgg atg cta tga ccatgcatac aagttgcaac taacaattaa cattttgaag      824
242 Thr Trp Met Leu
243          260
245 cctgtactcc tcaatgagct c      845
248 <210> SEQ ID NO: 4
249 <211> LENGTH: 260
250 <212> TYPE: PRT
251 <213> ORGANISM: Babesia canis
253 <400> SEQUENCE: 4
255 Val Asp Thr Ser Glu Asn Ser Leu Val Leu Ile Leu Ser Leu Phe Thr
256 1          5          10          15
259 Met Lys Gly Phe Phe Gly Ile Ile Leu Ser Ile Ile Phe Val Arg Ala
260          20          25          30
263 Val Ser Cys Thr Glu Asp Glu Asn Arg Asp Ser Val Val Glu Gly Ala
264          35          40          45
267 Thr Ser Val Glu Ala Ser Leu Lys Glu Gln Ile Asp Trp Leu Ala Glu
268          50          55          60
271 Arg Tyr Ser Ala Asp Leu Thr Asn Lys Asp Thr Ser Lys Trp Asn Thr
272 65          70          75          80
275 Glu Glu Gln Val Lys Glu Leu Leu Asn Glu Lys Ala Val Gly Ile Glu
276          85          90          95
279 Ser Arg Leu Leu Ala Ile Ala Lys Glu Phe His Lys Leu Lys Ser Val
280          100          105          110
283 Leu Cys Thr Gly Val Asn Glu Thr Pro Ala His Val Ala Asn Arg Val
284          115          120          125
287 Ser Pro Gly Asp Ala Ile Ser Met Leu Tyr Val Leu Pro Asn Thr His
288          130          135          140
291 Arg Glu Leu Ser Ser Leu Lys Asn Lys Ile Asp Glu Trp Lys Lys Val
292 145          150          155          160
295 Lys Ala Ser Asp Asn Gly Thr Asn Val Ile Lys Asn Ile Lys Asp Asp

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TIME: 13:27:45

Input Set : E:\2003-005.txt

Output Set: N:\CRF4\01192006\J563601.raw

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296          165          170          175
299 Arg Thr Asn Thr Trp Phe Val Ala His Gly Phe Lys Val Ala Glu Leu
300          180          185          190
303 Asn Asp Val Thr Leu Glu Lys Leu Ala Thr Val Val Lys Lys Leu Val
304          195          200          205
307 Ser His Lys Asp Met Lys Tyr Ile Asn Lys Val Met Lys Lys Tyr Phe
308          210          215          220
311 Asp Arg Gln Lys Lys Glu Ala Glu Arg Leu Thr Lys Lys Ala Glu Lys
312 225          230          235          240
315 Gly Met Ser Gly Gly Lys Tyr Lys Val Lys Gly Tyr Ala Ala Pro Ser
316          245          250          255
319 Thr Trp Met Leu
320          260
323 <210> SEQ ID NO: 5
324 <211> LENGTH: 21
325 <212> TYPE: DNA
326 <213> ORGANISM: Artificial
328 <220> FEATURE:
329 <223> OTHER INFORMATION: Primer
331 <400> SEQUENCE: 5
332 tgatgaagcc ggcaagaagg t
335 <210> SEQ ID NO: 6
336 <211> LENGTH: 22
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Primer
343 <400> SEQUENCE: 6
344 tacatgatac cgaattcaat gg
347 <210> SEQ ID NO: 7
348 <211> LENGTH: 27
349 <212> TYPE: DNA
350 <213> ORGANISM: Artificial
352 <220> FEATURE:
353 <223> OTHER INFORMATION: Primer
355 <400> SEQUENCE: 7
356 ttacatcggt gagctcagct accttga
359 <210> SEQ ID NO: 8
360 <211> LENGTH: 22
361 <212> TYPE: DNA
362 <213> ORGANISM: Artificial
364 <220> FEATURE:
365 <223> OTHER INFORMATION: Primer
367 <400> SEQUENCE: 8
368 ccatggattc aaggtagctg ag
371 <210> SEQ ID NO: 9
372 <211> LENGTH: 21
373 <212> TYPE: DNA
374 <213> ORGANISM: Artificial

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/563,601

DATE: 01/19/2006
TIME: 13:27:46

Input Set : E:\2003-005.txt
Output Set: N:\CRF4\01192006\J563601.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19

VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/563,601**

DATE: 01/19/2006

TIME: 13:27:46

Input Set : **E:\2003-005.txt**

Output Set: **N:\CRF4\01192006\J563601.raw**

L:7 M:201 W: Mandatory field data missing, <130> FILE REFERENCE

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date